

Amendments to the Specification:

Please replace the paragraph on page 24, lines 16-30, with the following paragraph:

A “substantial portion” of an amino acid or nucleotide sequence comprises enough of the amino acid sequence of a polypeptide or the nucleotide sequence of a gene to putatively identify that polypeptide or gene, either by manual evaluation of the sequence by one skilled in the art, or by computer-automated sequence comparison and identification using algorithms such as BLAST (Basic Local Alignment Search Tool; Altschul, S.F., *et al.*, (1993) *J. Mol. Biol.* 215: 403-410). In general, a sequence of ten or more contiguous amino acids or thirty or more nucleotides is necessary in order to putatively identify a polypeptide or nucleic acid sequence as homologous to a known protein or gene. Moreover, with respect to nucleotide sequences, gene specific oligonucleotide probes comprising 20-30 contiguous nucleotides may be used in sequence-dependent methods of gene identification (e.g., Southern hybridization) and isolation (e.g., *in situ* hybridization of bacterial colonies or bacteriophage plaques). In addition, short oligonucleotides of 12-15 bases may be used as amplification primers in PCR in order to obtain a particular nucleic acid fragment comprising the primers. Accordingly, a “substantial portion” of a nucleotide sequence comprises enough of the sequence to specifically identify and/or isolate a nucleic acid fragment comprising the sequence.

Please replace the paragraph on page 17, lines 16-31, with the following paragraph:

The term “response element” means one or more cis-acting DNA elements which confer responsiveness on a promoter mediated through interaction with the DNA-binding domains of the first chimeric gene. This DNA element may be either palindromic (perfect or imperfect) in its sequence or composed of sequence motifs or half sites separated by a variable number of nucleotides. The half sites can be similar or identical and arranged as either direct or inverted repeats or as a single half site or multimers of adjacent half sites in tandem. The response element may comprise a minimal promoter isolated from different organisms depending upon the nature of the cell or organism into which the response element will be incorporated. The DNA binding domain of the first hybrid protein binds, in the presence or absence of a ligand, to the DNA sequence of a response element to initiate or suppress transcription of downstream gene(s) under the regulation of this response element. Examples of DNA sequences for response elements of the natural ecdysone receptor include: RRGG/TTCANTGAC/ACY (SEQ ID NO: 17) (see Cherbas L., *et. al.*, (1991), *Genes Dev.* 5, 120-131); AGGTCAN_(n)AGGTCA, where N_(n) can be one or more spacer nucleotides (SEQ ID NO: 18) (see D'Avino PP., *et. al.*, (1995), *Mol. Cell. Endocrinol.* 113, 1-9); and

Application No. 09/965,697
Response dated January 10, 2006
Reply to Office Action dated July 12, 2005

GGGTTGAATGAATTT (SEQ ID NO: 19) (see Antoniewski C., et. al., (1994). *Mol. Cell Biol.* 14, 4465-4474).